

1 ATGAAGTTGCCTGTTAGGCTGTTGGTGCTTCTGTTGTTCTGGATTCTGTTTCCGGAGGT 60  
 -----  
 TACTTCAACGGACAATCCGACAACCACGAAGACAACAAGACCTAAGGACAAAGGCCTCCA  
 [M K L P V R L L V L L L F W I P V S G G]

Signal Peptide

61 GATGTTGTGGTGACTCAAACCTCCACTCTCCCTGCCTGTCAGCTTGGAGATCAAGTTTCT 120  
 -----  
 CTACAACACCACTGAGTTTGAGGTGAGAGGGACGGACAGTCGAAACCTCTAGTTCAAAGA  
 [D V V V T Q T P L S L P V S F G D Q V S]

Framework 1

121 ATCTCTTGCAGGTCTAGTCAGAGTCTTGCAAAGAGTTATGGGAACACCTATTTGTCTTGG 180  
 -----  
 TAGAGAACGTCCAGATCAGTCTCAGAACGTTTCTCAATACCCTGTGGATAAACAGAACC  
 I S C][R S S Q S L A K S Y G N T Y L S][W

CDR 1

181 TACCTGCACAAGCCTGGCCAGTCTCCACAGCTCCTCATCTATGGGATTTCCAACAGATTT 240  
 -----  
 ATGGACGTGTTTCGGACCGGTCAGAGGTGTCGAGGAGTAGATACCCTAAAGGTTGTCTAAA  
 Y L H K P G Q S P Q L L I Y][G I S N R F

Framework 2

CDR 2

241 TCTGGGGTGCCAGACAGGTTCACTGGCAGTGGTTCAGGGACAGATTTCACTCAAGATC 300  
 -----  
 AGACCCACGGTCTGTCCAAGTCACCGTCACCAAGTCCCTGTCTAAAGTGTGAGTTCTAG  
 S][G V P D R F S G S G S G T D F T L K I

Framework 3

301 AGCACAATAAAGCCTGAGGACTTGGGAATGTATTACTGCTTACAAGGTACACATCAGCCG 360  
 -----  
 TCGTGTTATTTTCGGACTCCTGAACCCTTACATAATGACGAATGTTCCATGTGTAGTCGGC  
 S T I K P E D L G M Y Y C][L Q G T H Q P

CDR 3

361 TACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA  
 -----  
 ATGTGCAAGCCTCCCCCTGTTTCGACCTTTATTTT  
 Y T][F G G G T K L E I K]

Framework 4

FIG. 1

1 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTATCAACAGCTACAAGTGTCCACTCCCAG 60  
 -----  
 TACCCTACCTCGACATAGTAGGAGAAGAACCATAGTTGTCGATGTTTACAGGTGAGGGTC  
 M G W S C I I L F L V S T A T S V H S][Q  
 Signal Peptide  
 61 GTCCAACTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGACTTCAGTGAAGCTGTCC 120  
 -----  
 CAGGTTGACGTCGTCGGACCCCGACTCGAACACTTCGGACCCTGAAGTCACTTCGACAGG  
 V Q L Q Q P G A E L V K P G T S V K L S  
 Framework 1  
 121 TGCAAGGGTTATGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCT 180  
 -----  
 ACGTTCCCAATACCGATGTGGAAGTGGTCGATGACCTACGTGACCCACTTCGTCTCCGGA  
 C K G Y G Y T F T][S Y W M H][W V K Q R P  
 CDR 1  
 181 GGACAAGGCCTTGAGTGGATCGGAGAGATTGATCCTTCTGAGAGTAATACTAACTACAAT 240  
 -----  
 CCTGTTCCGGAACCTACCTAGCCTCTCTAACTAGGAAGACTCTCATTATGATTGATGTTA  
 G Q G L E W I G][E I D P S E S N T N Y N  
 Framework 2 CDR 2  
 241 CAAAAATTCAAGGGCAAGGCCACATTGACTGTAGACATTTCTCCAGCACAGCCTACATG 300  
 -----  
 GTTTTTTAAGTTCCCGTTCCGGTGTAAGTACATCTGTAAAGGAGGTCGTGTCGGATGTAC  
 Q K F K G][K A T L T V D I S S S T A Y M  
 Framework 3  
 301 CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTACTATTGTGCAAGAGGGGGTTAC 360  
 -----  
 GTCGAGTCGTCGGACTGTAGACTCCTGAGACGCCAGATGATAACACGTTCTCCCCCAATG  
 Q L S S L T S E D S A V Y Y C A R][G G Y  
 361 GACGGATGGGACTATGCTATTGACTACTGGGGTCAAGGCACCTCAGTCACCGTCTCCTCA 420  
 -----  
 CTGCCTACCCTGATACGATAACTGATGACCCAGTTCCGTGGAGTCAGTGGCAGAGGAGT  
 D G W D Y A I D Y][W G Q G T S V T V S S]  
 CDR 3 Framework 4

FIG. 2

10 20 30 40  
 \* \* \* \*  
 ATG AAA TGC ACC TGG GTC ATT CTC TTC TTG GTA TCA ACA GCT ACA AGT  
 M K C T W V I L F L V S T A T S>  
 signal peptide cleavage site  
 50 60 70 80 90  
 \* \* \* \* \*  
 GTC CAC TCC CAG GTC CAA CTA GTG CAG TCT GGG GCT GAG GTT AAG AAG  
 V H S Q V Q L V Q S G A E V K K  
 100 110 120 130 140  
 \* \* \* \* \*  
 CCT GGG GCT TCA GTG AAG GTG TCC TGC AAG GGT TCT GGC TAC ACC TTC  
 P G A S V K V S C K G S G Y T F>  
 Xba I  
 150 160 170 180 190  
 \* \* \* \* \*  
 ACC AGC TAC TGG ATG CAT TGG GTG AGG CAG GCG CCT GGC CAA CGT CTA  
 T S Y W M H V R Q A P G Q R L>  
 200 210 220 230 240  
 \* \* \* \* \*  
 GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT ACT AAC TAC AAT  
 E W I G E I D P S E S N T N Y N>  
 Nhe I  
 250 260 270 280 290  
 \* \* \* \* \*  
 CAA AAA TTC AAG GGA CGC GTC ACA TTG ACT GTA GAC ATT TCC GCT AGC  
 Q K F K G R V T L T V D I S A S>  
 300 310 320 330 340  
 \* \* \* \* \*  
 ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACT GCG GTC  
 T A Y M E L S S L R S E D T A V>  
 350 360 370 380 390  
 \* \* \* \* \*  
 TAC TAT TGT GCA AGA GGG GGT TAC GAC GGA TGG GAC TAT GCT ATT GAC  
 Y Y C A R G G Y D G W D Y A I D>  
 400 410 420 430 440  
 \* \* \* \* \*  
 TAC TGG GGT CAA GGC ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG  
 Y W G Q G T L V T V S S A S T K>  
 450 460 470 480 490  
 \* \* \* \* \*  
 GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG  
 G P S V F P L A P S S K S T S G>  
 500 510 520 530 540  
 \* \* \* \* \*  
 GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG  
 G T A A L G C L V K D Y F P E P>  
 \*Age I  
 550 560  
 \* \*  
 GTG ACG GTG TCG  
 V T V S>

FIG. 3

10                      20                      30                      40  
 \*                      \*                      \*                      \*  
 ATG AAG TTG CCT GTT AGG CTG TTG GTG CTT CTG TTG TTC TGG ATT CCT  
 M K L P V R L L V L L F W I P>  
 Signal peptide cleavage site  
 50      BspE I      60                      70                      80                      90  
 \*                      \*                      \*                      \*                      \*                      \*  
 GTT TCC GGA GGT GAT GTT GTG ATG ACT CAA AGT CCA CTC TCC CTG CCT  
 V S G G D V V M T Q S P L S L P>  
 100                      110                      120                      130                      140  
 \*                      \*                      \*                      \*                      \*  
 GTC ACC CCT GGA GAA CCA GCT TCT ATC TCT TGC AGG TCT AGT CAG AGT  
 V T P G E P A S I S C R S S Q S>  
 150                      160                      170                      180 Asp 718                      190  
 \*                      \*                      \*                      \*                      \*                      \*  
 CTT GCA AAG AGT TAT GGG AAC ACC TAT TTG TCT TGG TAC CTG CAG AAG  
 L A K S Y G N T Y L S W Y L Q K>  
 200                      210                      220                      230                      240  
 \*Msc I \*                      \*                      \*                      \*                      \*  
 CTT GGC CAG TCT CCA CAG CTC CTC ATC TAT GGG ATT TCC AAC AGA TTT  
 P G Q S P Q L L I Y G I S N R F>  
 250                      260                      270                      280  
 \*                      \*                      \*                      \*                      \*  
 TCT GGG GTG CCA GAC AGG TTC AGT GGC AGT GGT TCA GGG ACA GAT TTC  
 S G V P D R F S G S G S G T D F>  
 290                      300 NruI                      310                      320                      330  
 \*                      \*                      \*                      \*                      \*  
 ACA CTC AAG ATC TCG CGA GTA GAG GCT GAG GAC GTG GGA GTG TAT TAC  
 T L K I S R V E A E D V G V Y Y>  
 340                      350                      360                      370                      380  
 \*                      \*                      \*                      \*                      \*  
 TGC TTA CAA GGT ACA CAT CAG CCG TAC ACG TTC GGA CAG GGG ACC AAG  
 C L Q G T H Q P Y T F G Q G T K>  
 390                      400                      410 Kas I  
 \*                      \*                      \*                      \*  
 GTG GAA ATA AAA CGG GCT GAT GCG GCG CC  
 V E I K R A D A A P>

FIG. 4

Light Chain

CDR1 R S S Q S L A K S Y G N T Y L S

CDR2 G I S N R F S

CDR3 L Q G T H Q P Y T

Heavy Chain

CDR1 S Y W M H

CDR2 E I D P S E S N T N Y N Q K F K G

CDR3 G G Y D G W D Y A I D Y

FIG. 5

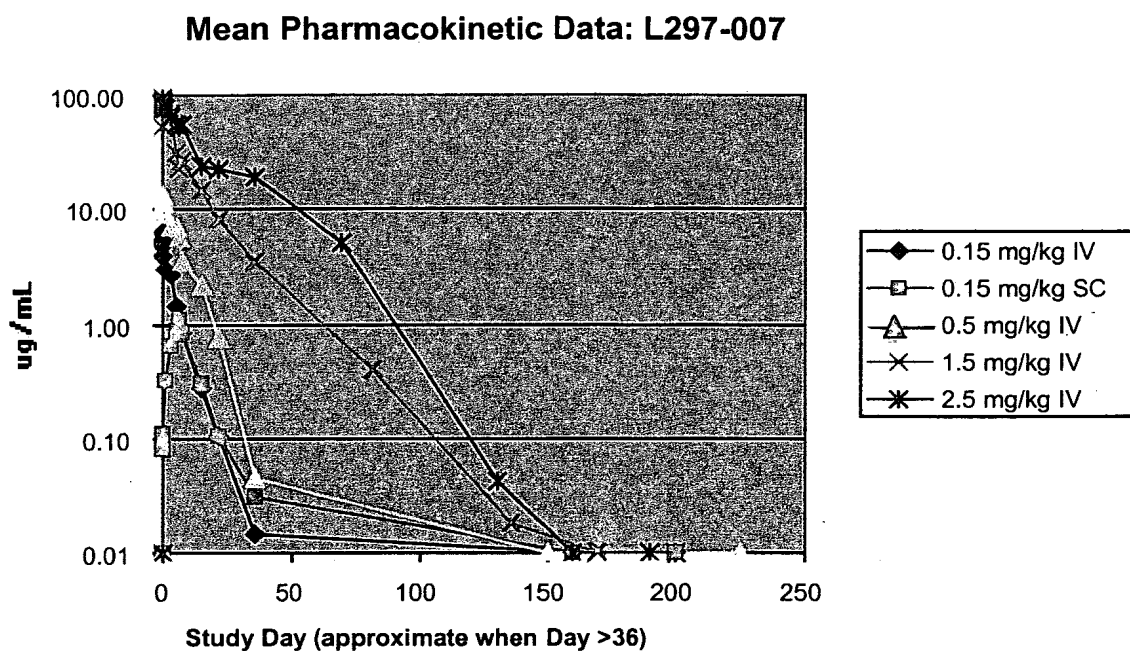


FIG. 6

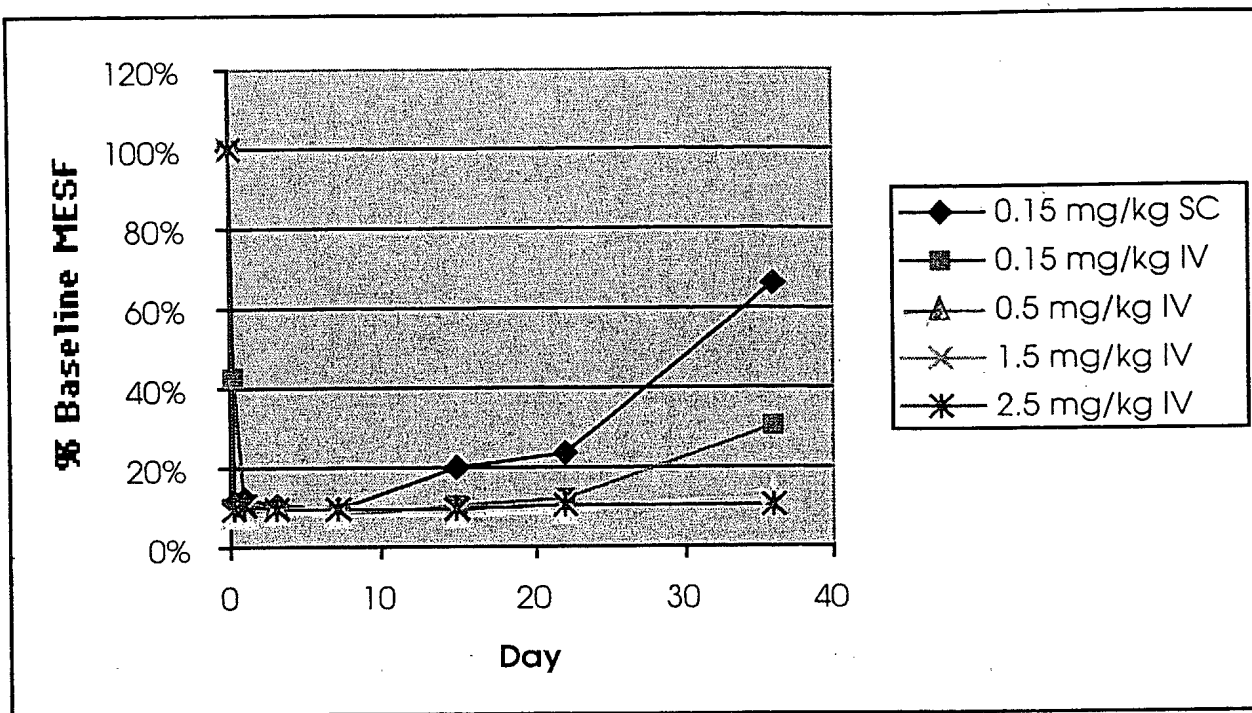


FIG. 7

# Mean Serum LDP-02 Profiles Phase Ib/IIa Study L297-006

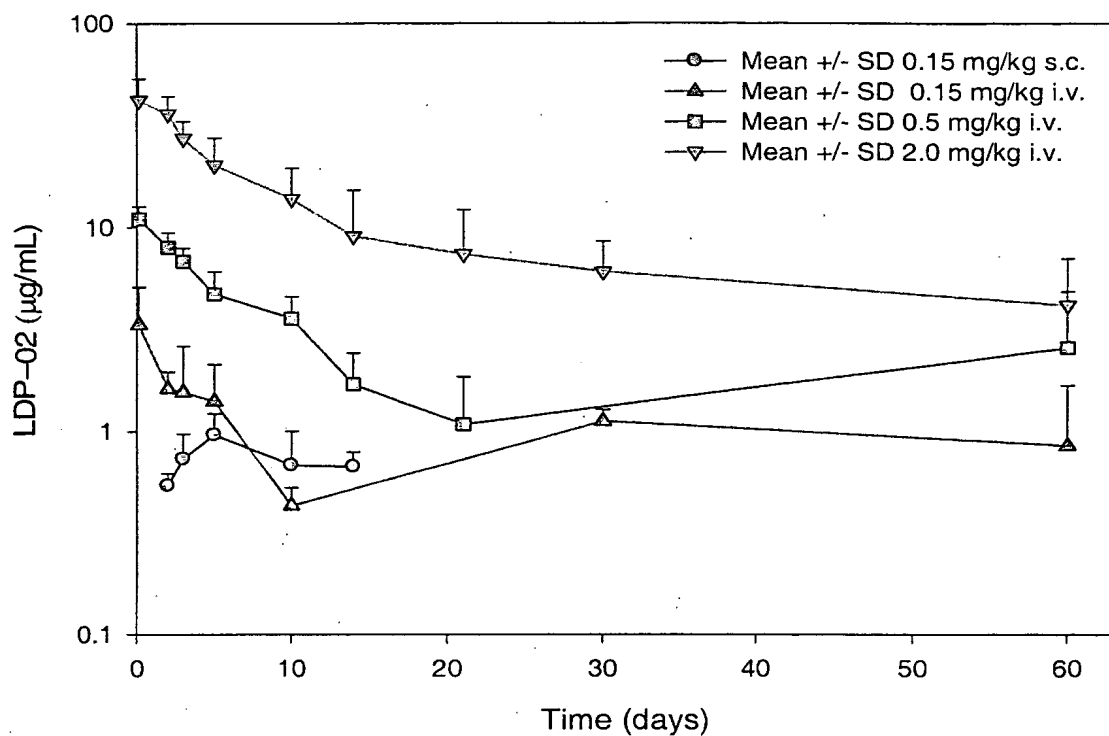


FIG. 8



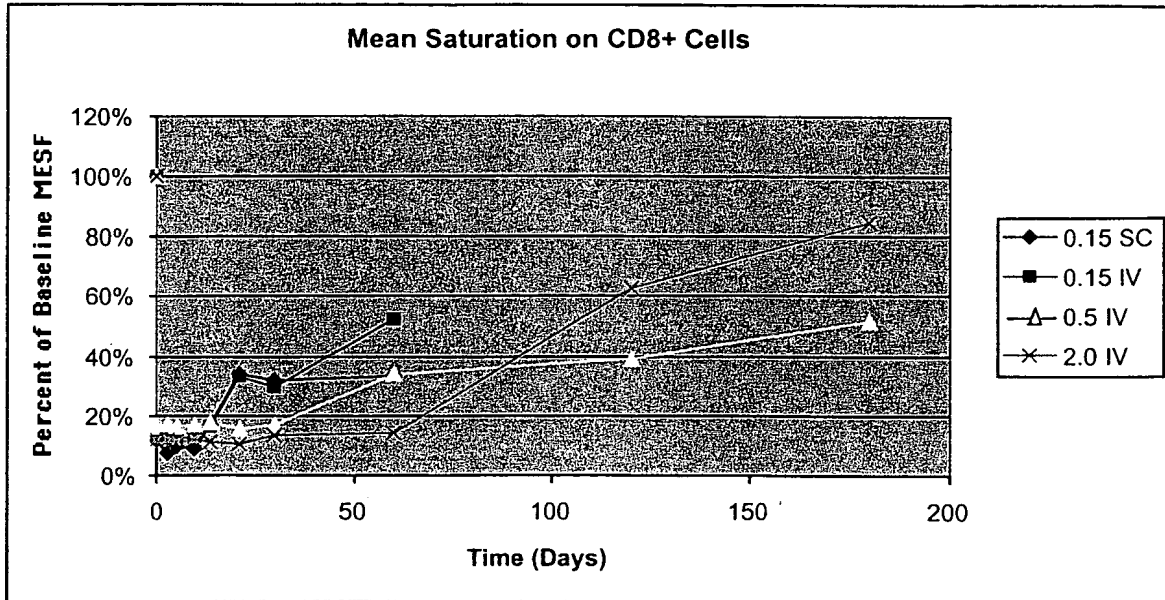


FIG. 9